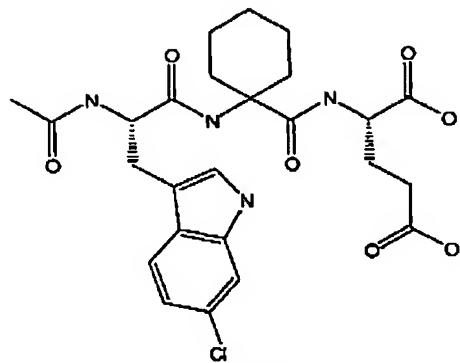


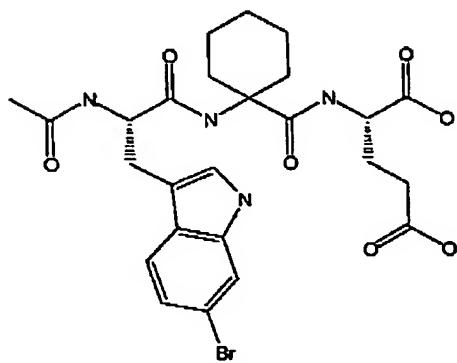
Amendment to the Claims: Please amend claims 1, 2, 15-17, 21 and 26-30 and cancel claims 3-5, 18-20, 24, 25 and 31-33 without prejudice as set forth below.

Listing of Claims: This listing replaces any previous listing.

1 (Currently Amended). A purified polypeptide comprising the amino acid sequence of SEQ ID NO: 4; wherein at least one of the seven variable positions of SEQ ID NO: 4 has an amino acid residue that differs from that of the corresponding wild-type Hdm2(17-125) amino acid sequence (SEQ ID NO: 2); and wherein ~~said polypeptide optionally comprises 1, 2, 3, 4, 5, 6, 7, 8, 9, 10 or 11 conservative amino acid substitutions that are not at one of the seven variable positions of SEQ ID NO: 4~~ wherein said polypeptide is soluble at a 34 mg/ml concentration and wherein said polypeptide is capable of binding a member selected from the group consisting of p53,



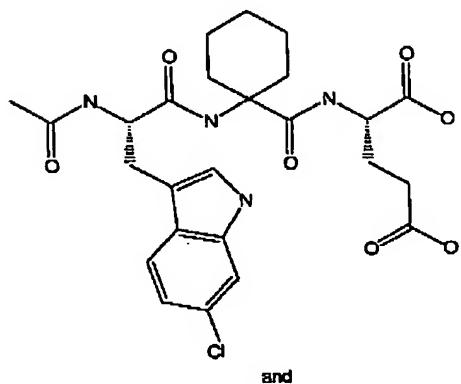
and



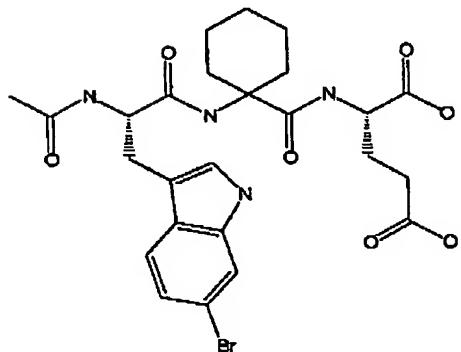
2 (Currently Amended). The polypeptide according to claim 1, wherein said polypeptide comprises an amino acid sequence selected from the group consisting of SEQ ID NO: 6, SEQ ID NO: 8, SEQ ID NO: 10 and SEQ ID NO: 12, ~~wherein any one of said amino acid sequences optionally comprises 1, 2, 3, 4, 5, 6, 7, 8, 9, 10 or 11 of said conservative amino acid substitutions.~~

3-13 (Cancelled).

14 (Original). A compound selected from the group consisting of



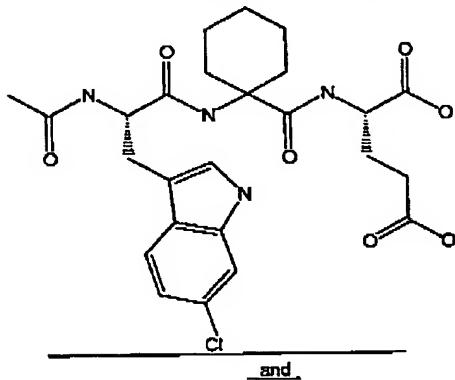
and



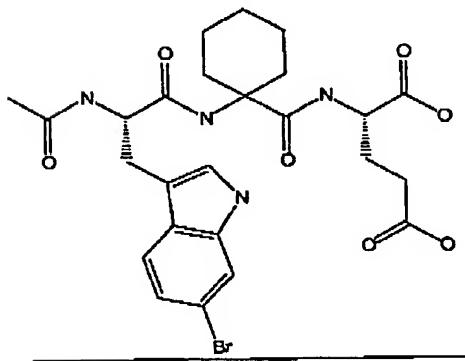
15 (Currently Amended). A polypeptide-compound complex comprising the compound according to claim 14 and a polypeptide complexed to it, wherein said polypeptide comprises the amino acid sequence of SEQ ID NO: 4, wherein at least one of the seven variable positions of SEQ ID NO: 4 has an amino acid residue that differs from that of the corresponding wild-type Hdm2(17-125) amino acid sequence (SEQ ID NO: 2), and wherein said polypeptide optionally comprises 1, 2, 3, 4, 5, 6, 7, 8, 9, 10 or 11 conservative amino acid substitutions that are not at one of the seven variable positions of SEQ ID NO: 4 wherein said polypeptide is soluble at a 34 mg/ml concentration.

16 (Currently Amended). A crystal comprising a polypeptide, wherein said polypeptide comprises the amino acid sequence of SEQ ID NO: 4, wherein at least one of the seven variable positions of SEQ ID NO: 4 has an amino acid residue that differs from that of the corresponding wild-

~~type Hdm2(17-125) amino acid sequence (SEQ ID NO: 2), and wherein said polypeptide optionally comprises 1, 2, 3, 4, 5, 6, 7, 8, 9, 10 or 11 conservative amino acid substitutions that are not at one of the seven variable positions of SEQ ID NO: 4 wherein said polypeptide is soluble at a 34 mg/ml concentration and wherein said polypeptide is capable of binding a member selected from the group consisting of p53,~~



and



17 (Currently Amended). The crystal according to claim 16, wherein said polypeptide comprises an amino acid sequence selected from the group consisting of SEQ ID NO: 6, SEQ ID NO: 8, SEQ ID NO: 10 and SEQ ID NO: 12, ~~wherein any one of said amino acid sequences optionally comprises 1, 2, 3, 4, 5, 6, 7, 8, 9, 10 or 11 of said conservative amino acid substitutions.~~

18 (Cancelled).

19 (Cancelled).

20 (Cancelled).

21 (Currently Amended). The crystal according to
~~either of claims~~ claim 16 or 20, wherein said crystal
effectively diffracts X-rays to a resolution of greater than
5.0 Å.

22 (Original). The crystal according to claim 21,
wherein said crystal effectively diffracts X-rays to a
resolution of greater than 2.5 Å.

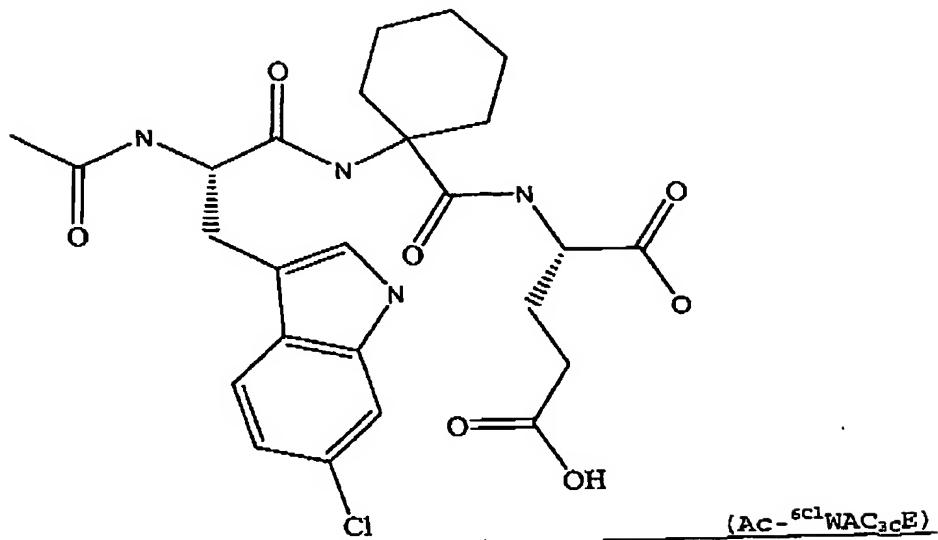
23 (Original). The crystal according to claim 22,
wherein said crystal effectively diffracts X-rays to a
resolution of greater than 1.5 Å.

24-25 (Cancelled).

26 (Currently Amended). The crystal according to
claim 16, wherein said polypeptide consists of the amino
acid of SEQ ID NO: 10 and said ~~crystal~~ polypeptide has the
structural coordinates as set forth in Table 3.

27 (Currently Amended). The crystal according to
claim 16, wherein said polypeptide consists of the amino
acid of SEQ ID NO: 6 and said ~~crystal~~ polypeptide has the
structural coordinates as set forth in Table 4.

28 (Currently Amended). A crystal comprising a
complex between a polypeptide and



, wherein said polypeptide is characterized by structure coordinates comprising a root mean square deviation (RMSD) of conserved residue backbone atoms of less than about 2.0 Å when superimposed on backbone atoms described by structural coordinates of Table 3 or Table 4.

29 (Currently Amended). The crystal according to claim 28, characterized by the structural coordinates set forth in Table 3 wherein said RMSD is less than about 1.5 Å.

30 (Currently Amended). The crystal according to claim 28 characterized by the structural coordinates set forth in Table 4 29, wherein said RMSD is less than about 1.0 Å.

31-33 (Cancelled).

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